LISTE DE SEQUENCES

5 <110> RHODIA CHIMIE
     CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
     (National Center for Scientific Research)

<120> METHOD FOR TRANSFORMING EPOXIDES CARRYING TRIFLUOROMETHYL GROUPS

10 <130> BFF 03P0374

<140>
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15 <160> 2

<170> PatentIn Ver. 2.1

<210> 1
20 <211> 1197
<212> ADN
<213> Aspergillus niger

<220>
25 <221> CDS
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Nucleotide sequence SEQ ID NO : 1
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   aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa   96
35 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
                   20   25   30

   acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg   144
   Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
40   35   40   45

   caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg   192
   Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
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45

   cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga   240
   Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
    65   70   75   80

50 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att   288
   Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
                       85   90   95

   cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca   336
55 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
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   ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg   384
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      Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
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      gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg     480
      Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
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      gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg     528
      Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
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      atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat     576
      Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
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      att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc     624
      Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
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      ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga     720
      Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
      225                 230                 235                 240

      atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt     768
      Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
                      245                 250                 255

      act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca     816
      Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
                      260                 265                 270

      tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc     864
      Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
                  275                 280                 285

      ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg     912
      Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
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      gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act     960
      Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
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      gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att    1008
      Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
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      cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg    1056
      His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
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      cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat    1104
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cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg   1152
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aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag       1197
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Peptide sequence SEQ ID NO : 2
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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
        35              40              45

Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
    50              55              60

Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
65              70              75              80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
            85              90              95

His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
            100             105             110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
        115             120             125

Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
    130             135             140

Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
145             150             155             160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
            165             170             175

Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
            180             185             190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
        195             200             205

Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
    210             215             220

Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
225             230             235             240
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Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
245   250   255

5 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
260   265   270

Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
275   280   285

10 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
290   295   300

Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
15 305   310   315   320

Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
325   330   335

20 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
340   345   350

Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
355   360   365

25 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
370   375   380

Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
30 385   390   395

35